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Synchronous improvement of subgenomes in rapeseed for Sclerotinia resistance

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Rapeseed (*Brassica napus*, AACC) is an important oilseed crop, containing two relative subgenomes, where homoelogenous genes interaction controls some important agronomy traits. Although high Sclerotinia resistance was identified in wild *B. oleracea* (CC) and the resistance can easily transferred into C subgenome of rapeseed (Ding et al. 2013; Mei et al. 2015), it was low efficiency to transfer resistance from C to A subgenome of rapeseed in vivo due to rare homoelogenous exchanges. Here we propose a breeding strategy of synchronous improvement Sclerotinia resistance in *B. napus*. First, a haploid hybrid between wild resistance *B. oleracea* (accession 'C01') and susceptible *B. rapa* (accession '6Y733') was backcrossed with '6Y733' for two times, and the progenies were screened with molecular markers linked with resistance loci together with resistance evaluation and chromosome behavior analysis. Then four groups of resynthesized *B. napus*, comprising of 37 lines with or without resistance loci from *B. rapa* and/or *B. oleracea* were developed for Sclerotinia resistance evaluation across three years. Significant differences were found among the four groups for both leaf and stem resistance. The group of resynthesized *B. napus* carrying resistance loci from *B. rapa* and *B. oleracea* (A+A+C+C+, the code of '+' means the genome carries resistance loci) exhibited the highest level of resistance, followed by A-A-C+C+, A+A+C-C- and A-A-C-C-. One of superior line showed 2.7-fold higher stem resistance than 'Zhongshuang 9', a partial resistant Chinese rapeseed variety. Our data highlights that the strategy of synchronous improvement of subgenomes can efficiently improve allopolyploids.

PLENARY TALKS

ORALS

POSTERS

WORKSHOPS